

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ARMITAGE, RICHARD
FANSLOW, WILLIAM
SPRIGGS, MELANIE
SRINIVASAN, SUBHASHINI
GIBSON, MARYLOU

(ii) TITLE OF INVENTION: NOVEL CYTOKINE

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: IMMUNEX CORPORATION
(B) STREET: 51 UNIVERSITY STREET
(C) CITY: SEATTLE
(D) STATE: WASHINGTON
(E) COUNTRY: USA
(F) ZIP: 98101

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Apple Operating System 7.1
(D) SOFTWARE: Microsoft Word for Apple, version 5.1a

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/969,703
(B) FILING DATE: October 23, 1992
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/805,723
(B) FILING DATE: December 5, 1991
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/783,707
(B) FILING DATE: October 25, 1991
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Perkins, Patricia A.
(B) REGISTRATION NUMBER: 34,693
(C) REFERENCE/DOCKET NUMBER: 2802-C

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 2065870430
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: MOUSE

(vii) IMMEDIATE SOURCE:

15

(B) CLONE: CD40-L

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..783

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

25	ATG ATA GAA ACA TAC AGC CAA CCT TCC CCC AGA TCC GTG GCA ACT GGA	48
	Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly	
	1 5 10 15	
30	CTT CCA GCG AGC ATG AAG ATT TTT ATG TAT TTA CTT ACT GTT TTC CTT	96
	Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu	
	20 25 30	
35	ATC ACC CAA ATG ATT GGA TCT GTG CTT TTT GCT GTG TAT CTT CAT AGA	144
	Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg	
	35 40 45	
40	AGA TTG GAT AAG GTC GAA GAG GAA GTA AAC CTT CAT GAA GAT TTT GTA	192
	Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val	
	50 55 60	
45	TTC ATA AAA AAG CTA AAG AGA TGC AAC AAA GGA GAA GGA TCT TTA TCC	240
	Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser	
	65 70 75 80	
50	TTG CTG AAC TGT GAG GAG ATG AGA AGG CAA TTT GAA GAC CTT GTC AAG	288
	Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys	
	85 90 95	
55	GAT ATA ACG TTA AAC AAA GAA GAG AAA AAA GAA AAC AGC TTT GAA ATG	336
	Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met	
	100 105 110	
60	CAA AGA GGT GAT GAG GAT CCT CAA ATT GCA GCA CAC GTT GTA AGC GAA	384
	Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu	
	115 120 125	
65	GCC AAC AGT AAT GCA GCA TCC GTT CTA CAG TGG GCC AAG AAA GGA TAT	432
	Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr	
	130 135 140	
70	TAT ACC ATG AAA AGC AAC TTG GTA ATG CTT GAA AAT GGG AAA CAG CTG	480
	Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu	
	145 150 155 160	

	ACG GTT AAA AGA GAA GGA CTC TAT TAT GTC TAC ACT CAA GTC ACC TTC	528
	Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe	
	165 170 175	
5	TGC TCT AAT CGG GAG CCT TCG AGT CAA CGC CCA TTC ATC GTC GGC CTC	576
	Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu	
	180 185 190	
10	TGG CTG AAG CCC AGC AGT GGA TCT GAG AGA ATC TTA CTC AAG GCG GCA	624
	Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala	
	195 200 205	
15	AAT ACC CAC AGT TCC TCC CAG CTT TGC GAG CAG CAG TCT GTT CAC TTG	672
	Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu	
	210 215 220	
20	GGC GGA GTG TTT GAA TTA CAA GCT GGT GCT TCT GTG TTT GTC AAC GTG	720
	Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val	
	225 230 235 240	
25	ACT GAA GCA AGC CAA GTG ATC CAC AGA GTT GGC TTC TCA TCT TTT GGC	768
	Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly	
	245 250 255	
30	TTA CTC AAA CTC TGA	783
	Leu Leu Lys Leu	
	260	
30	(2) INFORMATION FOR SEQ ID NO:2:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 260 amino acids	
	(B) TYPE: amino acid	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
40	Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly	
	1 5 10 15	
45	Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu	
	20 25 30	
	Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg	
	35 40 45	
50	Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val	
	50 55 60	
55	Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser	
	65 70 75 80	
	Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys	
	85 90 95	
60	Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met	
	100 105 110	
	Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu	
	115 120 125	

Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr
130 135 140

5 Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu
145 150 155 160

Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe
165 170 175

10 Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu
180 185 190

15 Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala
195 200 205

Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu
210 215 220

20 Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val
225 230 235 240

Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly
245 250 255

25 Leu Leu Lys Leu
260

30 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 740 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
45 (A) ORGANISM: HUMAN

(vii) IMMEDIATE SOURCE:
(B) CLONE: IgG1 Fc

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	CGGTACCGCT AGCGTCGACA GGCCTAGGAT ATCGATACGT AGAGCCCAGA TCTGTGACA	60
55	AAACTCACAC ATGCCCACCG TGCCAGCAC CTGAACTCCT GGGGGGACCG TCAGTCTTCC	120
	TCTTCCCCC AAAACCCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG GTCACATGCG	180
	TGGTGGTGGA CGTGAGCCAC GAAGACCCTG AGGTCAAGTT CAACTGGTAC GTGGACGGCG	240
60	TGGAGGTGCA TAATGCCAAG ACAAAGCCGC GGGAGGAGCA GTACAACAGC ACGTACCGGG	300
	TGGTCAGCGT CCTCACCGTC CTGCACCAGG ACTGGCTGAA TGGCAAGGAC TACAAGTGCA	360

5 AGGTCTCCAA CAAAGCCCTC CCAGCCCCCA TGCAGAAAAC CATCTCCAAA GCCAAAGGGC 420
 AGCCCCGAGA ACCACAGGTG TACACCCTGC CCCCATCCCG GGATGAGCTG ACCAAGAACC 480
 AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTATCCCAG GCACATCGCC GTGGAGTGGG 540
 AGAGCAATGG GCAGCCGGAG AACAACTACA AGACCACGCC TCCCGTGCTG GACTCCGACG 600
 10 GCTCCTTCTT CCTCTACAGC AAGCTCACCG TGGACAAGAG CAGGTGGCAG CAGGGGAACG 660
 TCTTCTCATG CTCCGTGATG CATGAGGCTC TGCACAACCA CTACACGCAG AAGAGCCTCT 720
 CCCTGTCTCC GGGTAAATGA 740

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HUMAN

(vii) IMMEDIATE SOURCE:

- (B) CLONE: CD40 EXTRACELLULAR REGION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 CAGAACACC CACTGCATGC AGAGAAAAAC AGTACCTAAT AAACAGTCAG TGCTGTTCTT 60
 TGTGCCAGCC AGGACAGAAA CTGGTGAGTG ACTGCACAGA GTTCACTGAA ACGGAATGCC 120
 TTCCTTGCGG TGAAAGCGAA TTCCTAGACA CCTGGAACAG AGAGACACAC TGCCACCAGC 180
 45 ACAAATACTG CGACCCCAAC CTAGGGCTTC GGTCCAGCA GAAGGGCACC TCAGAAACAG 240
 ACACCATCTG CACCTGTGAA GAAGGCTGGC ACTGTACGAG TGAGGCCTGT GAGAGCTGTG 300
 TCCTGCACCG CTCATGCTCG CCCGGCTTTG GGGTCAAGCA GATTGCTACA GGGGTTTCTG 360
 50 ATACCATCTG CGAGCCCTGC CCAGTCGGCT TCTTCTCCAA TGTGTCATCT GCTTTCGAAA 420
 AATGTCACCC TTGGACAAGC TGTGAGACCA AAGACCTGGT TGTGCAACAG GCAGGCACAA 480
 55 ACAAGACTGA TGTTGTCTGT GGTCCCCAGG ATCGGCTGA 519

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 10 (A) ORGANISM: PCR PRIMER
 (vii) IMMEDIATE SOURCE:
 (B) CLONE: CD40 5' PRIMER
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
 CCGTCGACCA CCATGGTTCG TCTGCC
 20 (2) INFORMATION FOR SEQ ID NO:6:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 30 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PCR PRIMER
 35 (vii) IMMEDIATE SOURCE:
 (B) CLONE: CD40 3' PRIMER
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
 CCGTCGACGT CTAGAGCCGA TCCTGGGG
 45 (2) INFORMATION FOR SEQ ID NO:7:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 55 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PCR PRIMER
 (vii) IMMEDIATE SOURCE:
 60 (B) CLONE: CD40 3' DOWNSTREAM PRIMER
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

26

28

ACAAGATCTG GGCTCTACGT ACTCAGCCGA TCCTGGGGAC

40

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PENTAPEPTIDE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Tyr Val Gly Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HUMAN IGG1/FC 5' PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TATTAATCAT TCAGTAGGGC CCAGATCTTG TGACAAAAC CAC

43

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:

(B) CLONE: HUMAN IGG1/FC 3' DOWNSTREAM PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCAGCTTAA CTAGTTCATT TACCCGGAGA CAGGGAGA

38

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 840 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: CD40-L

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 46..831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCCACCTTC TCTGCCAGAA GATACCATTT CAACTTTAAC ACAGC ATG ATC GAA
Met Ile Glu

54

1

ACA TAC AAC CAA ACT TCT CCC CGA TCT GCG GCC ACT GGA CTG CCC ATC
Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly Leu Pro Ile
5 10 15

102

AGC ATG AAA ATT TTT ATG TAT TTA CTT ACT GTT TTT CTT ATC ACC CAG
Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu Ile Thr Gln
20 25 30 35

150

ATG ATT GGG TCA GCA CTT TTT GCT GTG TAT CTT CAT AGA AGG TTG GAC
Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg Arg Leu Asp
40 45 50

198

AAG ATA GAA GAT GAA AGG AAT CTT CAT GAA GAT TTT GTA TTC ATG AAA
Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys
55 60 65

246

ACG ATA CAG AGA TGC AAC ACA GGA GAA AGA TCC TTA TCC TTA CTG AAC
Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn
70 75 80

294

TGT GAG GAG ATT AAA AGC CAG TTT GAA GGC TTT GTG AAG GAT ATA ATG
Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met

342

	85	90	95	
5	TTA AAC AAA GAG GAG ACG AAG AAA GAA AAC AGC TTT GAA ATG CAA AAA Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys 100 105 110 115	390		
10	GGT GAT CAG AAT CCT CAA ATT GCG GCA CAT GTC ATA AGT GAG GCC AGC Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser 120 125 130	438		
15	AGT AAA ACA ACA TCT GTG TTA CAG TGG GCT GAA AAA GGA TAC TAC ACC Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr 135 140 145	486		
20	ATG AGC AAC AAC TTG GTA ACC CTG GAA AAT GGG AAA CAG CTG ACC GTT Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val 150 155 160	534		
25	AAA AGA CAA GGA CTC TAT TAT ATC TAT GCC CAA GTC ACC TTC TGT TCC Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser 165 170 175	582		
30	AAT CGG GAA GCT TCG AGT CAA GCT CCA TTT ATA GCC AGC CTC TGC CTA Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu 180 185 190 195	630		
35	AAG TCC CCC GGT AGA TTC GAG AGA ATC TTA CTC AGA GCT GCA AAT ACC Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr 200 205 210	678		
40	CAC AGT TCC GCC AAA CCT TGC GGG CAA CAA TCC ATT CAC TTG GGA GGA His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly 215 220 225	726		
45	GTA TTT GAA TTG CAA CCA GGT GCT TCG GTG TTT GTC AAT GTG ACT GAT Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp 230 235 240	774		
50	CCA AGC CAA GTG AGC CAT GGC ACT GGC TTC ACG TCC TTT GGC TTA CTC Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu 245 250 255	822		
55	AAA CTC TGAACAGTGT CA Lys Leu 260	840		

(2) INFORMATION FOR SEQ ID NO:12:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

60	Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly 1 5 10 15
	Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu 20 25 30

	Ile	Thr	Gln	Met	Ile	Gly	Ser	Ala	Leu	Phe	Ala	Val	Tyr	Leu	His	Arg	
			35					40					45				
5	Arg	Leu	Asp	Lys	Ile	Glu	Asp	Glu	Arg	Asn	Leu	His	Glu	Asp	Phe	Val	
		50					55					60					
	Phe	Met	Lys	Thr	Ile	Gln	Arg	Cys	Asn	Thr	Gly	Glu	Arg	Ser	Leu	Ser	
	65					70					75					80	
10	Leu	Leu	Asn	Cys	Glu	Glu	Ile	Lys	Ser	Gln	Phe	Glu	Gly	Phe	Val	Lys	
					85					90					95		
	Asp	Ile	Met	Leu	Asn	Lys	Glu	Glu	Thr	Lys	Lys	Glu	Asn	Ser	Phe	Glu	
15				100					105					110			
	Met	Gln	Lys	Gly	Asp	Gln	Asn	Pro	Gln	Ile	Ala	Ala	His	Val	Ile	Ser	
			115					120					125				
20	Glu	Ala	Ser	Ser	Lys	Thr	Thr	Ser	Val	Leu	Gln	Trp	Ala	Glu	Lys	Gly	
		130					135					140					
	Tyr	Tyr	Thr	Met	Ser	Asn	Asn	Leu	Val	Thr	Leu	Glu	Asn	Gly	Lys	Gln	
	145					150					155					160	
25	Leu	Thr	Val	Lys	Arg	Gln	Gly	Leu	Tyr	Tyr	Ile	Tyr	Ala	Gln	Val	Thr	
				165					170						175		
	Phe	Cys	Ser	Asn	Arg	Glu	Ala	Ser	Ser	Gln	Ala	Pro	Phe	Ile	Ala	Ser	
30				180					185					190			
	Leu	Cys	Leu	Lys	Ser	Pro	Gly	Arg	Phe	Glu	Arg	Ile	Leu	Leu	Arg	Ala	
			195					200					205				
35	Ala	Asn	Thr	His	Ser	Ser	Ala	Lys	Pro	Cys	Gly	Gln	Gln	Ser	Ile	His	
		210					215					220					
	Leu	Gly	Gly	Val	Phe	Glu	Leu	Gln	Pro	Gly	Ala	Ser	Val	Phe	Val	Asn	
	225					230					235					240	
40	Val	Thr	Asp	Pro	Ser	Gln	Val	Ser	His	Gly	Thr	Gly	Phe	Thr	Ser	Phe	
					245					250					255		
	Gly	Leu	Leu	Lys	Leu												
45				260													

(2) INFORMATION FOR SEQ ID NO:13:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- 60 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGGTGGCGGA GGGTCAGGCG GAGGTGGGTC CGGAGGCGGG GGTCAAGTT CTGACAAGAT 60
5 AGAAGATGAA AGG 73

(2) INFORMATION FOR SEQ ID NO:14:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

20 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

25 GGCCGCTCAG AGTTTGAGTA A 21

(2) INFORMATION FOR SEQ ID NO:15:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

40 (iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: Human CD40-L/FC2 (soluble CD40-L)

45 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 4..1422

50 (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 79..1422

55 (ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 4..78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

60 TAT ATG TTC CAT GTT TCT TTT AGA TAT ATC TTT GGA ATT CCT CCA CTG 48
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu
-25 -20 -15

	ATC CTT GTT CTG CTG CCT GTC ACT AGC TCT GAC TAC AAA GAT GAC GAT Ile Leu Val Leu Leu Pro Val Thr Ser Ser Asp Tyr Lys Asp Asp Asp -10 -5 1 5	96
5	GAT AAA AGA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA Asp Lys Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala 10 15 20	144
10	CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro 25 30 35	192
15	AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val 40 45 50	240
20	GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val 55 60 65 70	288
25	GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln 75 80 85	336
30	TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln 90 95 100	384
35	GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala 105 110 115	432
40	CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro 120 125 130	480
45	CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr 135 140 145 150	528
50	AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser 155 160 165	576
55	GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr 170 175 180	624
60	AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr 185 190 195	672
65	AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe 200 205 210	720
70	TCA TGC TCC GTG ATG CAT GGT GGC GGA GGG TCA GGC GGA GGT GGG TCC Ser Cys Ser Val Met His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser 215 220 225 230	768
75	GGA GGC GGG GGT TCA AGT TCT GAC AAG ATA GAA GAT GAA AGG AAT CTT Gly Gly Gly Gly Ser Ser Ser Asp Lys Ile Glu Asp Glu Arg Asn Leu 235 240 245	816

	CAT GAA GAT TTT GTA TTC ATG AAA ACG ATA CAG AGA TGC AAC ACA GGA	864
	His Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly	
	250 255 260	
5	GAA AGA TCC TTA TCC TTA CTG AAC TGT GAG GAG ATT AAA AGC CAG TTT	912
	Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe	
	265 270 275	
10	GAA GGC TTT GTG AAG GAT ATA ATG TTA AAC AAA GAG GAG ACG AAG AAA	960
	Glu Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys	
	280 285 290	
15	GAA AAC AGC TTT GAA ATG CAA AAA GGT GAT CAG AAT CCT CAA ATT GCG	1008
	Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala	
	295 300 305 310	
20	GCA CAT GTC ATA AGT GAG GCC AGC AGT AAA ACA ACA TCT GTG TTA CAG	1056
	Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln	
	315 320 325	
	TGG GCT GAA AAA GGA TAC TAC ACC ATG AGC AAC AAC TTG GTA ACC CTG	1104
	Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu	
	330 335 340	
25	GAA AAT GGG AAA CAG CTG ACC GTT AAA AGA CAA GGA CTC TAT TAT ATC	1152
	Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile	
	345 350 355	
30	TAT GCC CAA GTC ACC TTC TGT TCC AAT CGG GAA GCT TCG AGT CAA GCT	1200
	Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala	
	360 365 370	
35	CCA TTT ATA GCC AGC CTC TGC CTA AAG TCC CCC GGT AGA TTC GAG AGA	1248
	Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg	
	375 380 385 390	
40	ATC TTA CTC AGA GCT GCA AAT ACC CAC AGT TCC GCC AAA CCT TGC GGG	1296
	Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly	
	395 400 405	
	CAA CAA TCC ATT CAC TTG GGA GGA GTA TTT GAA TTG CAA CCA GGT GCT	1344
	Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala	
	410 415 420	
45	TCG GTG TTT GTC AAT GTG ACT GAT CCA AGC CAA GTG AGC CAT GGC ACT	1392
	Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr	
	425 430 435	
50	GGC TTC ACG TCC TTT GGC TTA CTC AAA CTC TGA	1425
	Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu	
	440 445	

55 (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 473 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
-25 -20 -15 -10
5 Leu Val Leu Leu Pro Val Thr Ser Ser Asp Tyr Lys Asp Asp Asp Asp
-5 1 5
10 Lys Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
10 15 20
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
25 30 35
15 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
40 45 50 55
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
60 65 70
20 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
75 80 85
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
90 95 100
25 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
105 110 115
30 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
120 125 130 135
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
140 145 150
35 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
155 160 165
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
170 175 180
40 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
185 190 195
45 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
200 205 210 215
Cys Ser Val Met His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
220 225 230
50 Gly Gly Gly Ser Ser Ser Asp Lys Ile Glu Asp Glu Arg Asn Leu His
235 240 245
Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu
250 255 260
55 Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu
265 270 275
60 Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu
280 285 290 295
Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala

300

305

310

His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp
 315 320 325

5 Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu
 330 335 340

10 Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr
 345 350 355

Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro
 360 365 370 375

15 Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile
 380 385 390

Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln
 395 400 405

20 Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser
 410 415 420

25 Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly
 425 430 435

Phe Thr Ser Phe Gly Leu Leu Lys Leu
 440 445

30 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
 1 5 10 15

45 Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
 20 25 30

Arg

50

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: DNA

60

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATATGAATTC GACTACAAAG ATGACGATGA TAAACCTCAA ATTGCAGCAC ACGTT

21

(2) INFORMATION FOR SEQ ID NO:19:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTTCGCGGC CGCGTTCAGA GTTTGAGTAA GCCAA

35

(2) INFORMATION FOR SEQ ID NO:20:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 929 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: Human CD40-L trimer

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 65..142

45 (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 65..886

50 (ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 143..886

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGAGCGAGTC CGCATCGACG GATCGGAAAA CCTCTCCGAG GTACCTATCC CGGGGATCCC

60

60 CACC ATG TTC CAT GTT TCT TTT AGA TAT ATC TTT GGA ATT CCT CCA CTG
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu
-26 -25 -20 -15

109

ATC CTT GTT CTG CTG CCT GTC ACT AGT TCT GAC CGT ATG AAA CAG ATA

157

	Ile	Leu	Val	Leu	Leu	Pro	Val	Thr	Ser	Ser	Asp	Arg	Met	Lys	Gln	Ile	
	-10						-5					1				5	
5	GAG	GAT	AAG	ATC	GAA	GAG	ATC	CTA	AGT	AAG	ATT	TAT	CAT	ATA	GAG	AAT	205
	Glu	Asp	Lys	Ile	Glu	Glu	Ile	Leu	Ser	Lys	Ile	Tyr	His	Ile	Glu	Asn	
					10					15					20		
10	GAA	ATC	GCC	CGT	ATC	AAA	AAG	CTG	ATT	GGC	GAG	CGG	ACT	AGT	TCT	GAC	253
	Glu	Ile	Ala	Arg	Ile	Lys	Lys	Leu	Ile	Gly	Glu	Arg	Thr	Ser	Ser	Asp	
				25				30					35				
15	AAG	ATA	GAA	GAT	GAA	AGG	AAT	CTT	CAT	GAA	GAT	TTT	GTA	TTC	ATG	AAA	301
	Lys	Ile	Glu	Asp	Glu	Arg	Asn	Leu	His	Glu	Asp	Phe	Val	Phe	Met	Lys	
			40				45						50				
20	ACG	ATA	CAG	AGA	TGC	AAC	ACA	GGA	GAA	AGA	TCC	TTA	TCC	TTA	CTG	AAC	349
	Thr	Ile	Gln	Arg	Cys	Asn	Thr	Gly	Glu	Arg	Ser	Leu	Ser	Leu	Leu	Asn	
		55					60					65					
25	TGT	GAG	GAG	ATT	AAA	AGC	CAG	TTT	GAA	GGC	TTT	GTG	AAG	GAT	ATA	ATG	397
	Cys	Glu	Glu	Ile	Lys	Ser	Gln	Phe	Glu	Gly	Phe	Val	Lys	Asp	Ile	Met	
		70				75					80					85	
30	TTA	AAC	AAA	GAG	GAG	ACG	AAG	AAA	GAA	AAC	AGC	TTT	GAA	ATG	CAA	AAA	445
	Leu	Asn	Lys	Glu	Glu	Thr	Lys	Lys	Glu	Asn	Ser	Phe	Glu	Met	Gln	Lys	
					90					95					100		
35	GGT	GAT	CAG	AAT	CCT	CAA	ATT	GCG	GCA	CAT	GTC	ATA	AGT	GAG	GCC	AGC	493
	Gly	Asp	Gln	Asn	Pro	Gln	Ile	Ala	Ala	His	Val	Ile	Ser	Glu	Ala	Ser	
				105				110						115			
40	AGT	AAA	ACA	ACA	TCT	GTG	TTA	CAG	TGG	GCT	GAA	AAA	GGA	TAC	TAC	ACC	541
	Ser	Lys	Thr	Thr	Ser	Val	Leu	Gln	Trp	Ala	Glu	Lys	Gly	Tyr	Tyr	Thr	
			120				125						130				
45	ATG	AGC	AAC	AAC	TTG	GTA	ACC	CTG	GAA	AAT	GGG	AAA	CAG	CTG	ACC	GTT	589
	Met	Ser	Asn	Asn	Leu	Val	Thr	Leu	Glu	Asn	Gly	Lys	Gln	Leu	Thr	Val	
		135					140					145					
50	AAA	AGA	CAA	GGA	CTC	TAT	TAT	ATC	TAT	GCC	CAA	GTC	ACC	TTC	TGT	TCC	637
	Lys	Arg	Gln	Gly	Leu	Tyr	Tyr	Ile	Tyr	Ala	Gln	Val	Thr	Phe	Cys	Ser	
		150				155					160					165	
55	AAT	CGG	GAA	GCT	TCG	AGT	CAA	GCT	CCA	TTT	ATA	GCC	AGC	CTC	TGC	CTA	685
	Asn	Arg	Glu	Ala	Ser	Ser	Gln	Ala	Pro	Phe	Ile	Ala	Ser	Leu	Cys	Leu	
				170						175					180		
60	AAG	TCC	CCC	GGT	AGA	TTC	GAG	AGA	ATC	TTA	CTC	AGA	GCT	GCA	AAT	ACC	733
	Lys	Ser	Pro	Gly	Arg	Phe	Glu	Arg	Ile	Leu	Leu	Arg	Ala	Ala	Asn	Thr	
				185					190					195			
65	CAC	AGT	TCC	GCC	AAA	CCT	TGC	GGG	CAA	CAA	TCC	ATT	CAC	TTG	GGA	GGA	781
	His	Ser	Ser	Ala	Lys	Pro	Cys	Gly	Gln	Gln	Ser	Ile	His	Leu	Gly	Gly	
			200				205						210				
70	GTA	TTT	GAA	TTG	CAA	CCA	GGT	GCT	TCG	GTG	TTT	GTC	AAT	GTG	ACT	GAT	829
	Val	Phe	Glu	Leu	Gln	Pro	Gly	Ala	Ser	Val	Phe	Val	Asn	Val	Thr	Asp	
		215					220					225					
75	CCA	AGC	CAA	GTG	AGC	CAT	GGC	ACT	GGC	TTC	ACG	TCC	TTT	GGC	TTA	CTC	877
	Pro	Ser	Gln	Val	Ser	His	Gly	Thr	Gly	Phe	Thr	Ser	Phe	Gly	Leu	Leu	
		230				235					240					245	

5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
-26 -25 -20 -15
Leu Val Leu Leu Pro Val Thr Ser Ser Asp Arg Met Lys Gln Ile Glu
-10 -5 1 5
Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu
10 15 20
Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Ser Ser Asp Lys
25 25 30 35
Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr
30 40 45 50
Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys
55 60 65 70
Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu
75 80 85
Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly
90 95 100
Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser
105 110 115
Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met
120 125 130
Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys
135 140 145 150
Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn
155 160 165
Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys
170 175 180
Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His
185 190 195
Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val
200 205 210
Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro
215 220 225 230

Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys
235 240 245

5 Leu

(2) INFORMATION FOR SEQ ID NO:22:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 878 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(B) CLONE: Murine CD40-L trimer

20 (ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 15..92

25 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 15..857

30 (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 93..857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

35 CTCGAGGTAC CGCC ATG TTC CAT GTT TCT TTT AGA TAT ATC TTT GGA ATT 50
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile
-26 -25 -20 -15

40 CCT CCA CTG ATC CTT GTT CTG CTG CCT GTC ACT AGT TCT GAC CGT ATG 98
Pro Pro Leu Ile Leu Val Leu Leu Pro Val Thr Ser Ser Asp Arg Met
-10 -5 1

45 AAA CAG ATA GAG GAT AAG ATC GAA GAG ATC CTA AGT AAG ATT TAT CAT 146
Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His
5 10 15

50 ATA GAG AAT GAA ATC GCC CGT ATC AAA AAG CTG ATT GGC GAG CGG ACT 194
Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr
20 25 30

AGT TCT GAC TAC AAA GAT GAC GAT GAT AAA GAT AAG GTC GAA GAG GAA 242
Ser Ser Asp Tyr Lys Asp Asp Asp Asp Lys Asp Lys Val Glu Glu Glu
35 40 45 50

55 GTA AAC CTT CAT GAA GAT TTT GTA TTC ATA AAA AAG CTA AAG AGA TGC 290
Val Asn Leu His Glu Asp Phe Val Phe Ile Lys Lys Leu Lys Arg Cys
55 60 65

60 AAC AAA GGA GAA GGA TCT TTA TCC TTG CTG AAC TGT GAG GAG ATG AGA 338
Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys Glu Glu Met Arg
70 75 80

	AGG CAA TTT GAA GAC CTT GTC AAG GAT ATA ACG TTA AAC AAA GAA GAG	386
	Arg Gln Phe Glu Asp Leu Val Lys Asp Ile Thr Leu Asn Lys Glu Glu	
	85 90 95	
5	AAA AAA GAA AAC AGC TTT GAA ATG CAA AGA GGT GAT GAG GAT CCT CAA	434
	Lys Lys Glu Asn Ser Phe Glu Met Gln Arg Gly Asp Glu Asp Pro Gln	
	100 105 110	
10	ATT GCA GCA CAC GTT GTA AGC GAA GCC AAC AGT AAT GCA GCA TCC GTT	482
	Ile Ala Ala His Val Val Ser Glu Ala Asn Ser Asn Ala Ala Ser Val	
	115 120 125 130	
15	CTA CAG TGG GCC AAG AAA GGA TAT TAT ACC ATG AAA AGC AAC TTG GTA	530
	Leu Gln Trp Ala Lys Lys Gly Tyr Tyr Thr Met Lys Ser Asn Leu Val	
	135 140 145	
20	ATG CTT GAA AAT GGG AAA CAG CTG ACG GTT AAA AGA GAA GGA CTC TAT	578
	Met Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Glu Gly Leu Tyr	
	150 155 160	
25	TAT GTC TAC ACT CAA GTC ACC TTC TGC TCT AAT CGG GAG CCT TCG AGT	626
	Tyr Val Tyr Thr Gln Val Thr Phe Cys Ser Asn Arg Glu Pro Ser Ser	
	165 170 175	
30	CAA CGC CCA TTC ATC GTC GGC CTC TGG CTG AAG CCC AGC AGT GGA TCT	674
	Gln Arg Pro Phe Ile Val Gly Leu Trp Leu Lys Pro Ser Ser Gly Ser	
	180 185 190	
35	GAG AGA ATC TTA CTC AAG GCG GCA AAT ACC CAC AGT TCC TCC CAG CTT	722
	Glu Arg Ile Leu Leu Lys Ala Ala Asn Thr His Ser Ser Ser Gln Leu	
	195 200 205 210	
40	TGC GAG CAG CAG TCT GTT CAC TTG GGC GGA GTG TTT GAA TTA CAA GCT	770
	Cys Glu Gln Gln Ser Val His Leu Gly Gly Val Phe Glu Leu Gln Ala	
	215 220 225	
45	GGT GCT TCT GTG TTT GTC AAC GTG ACT GAA GCA AGC CAA GTG ATC CAC	818
	Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln Val Ile His	
	230 235 240	
50	AGA GTT GGC TTC TCA TCT TTT GGC TTA CTC AAA CTC TGAACGCGGC	864
	Arg Val Gly Phe Ser Ser Phe Gly Leu Leu Lys Leu	
	245 250 255	
55	CGCTACAGAT CTAC	878

(2) INFORMATION FOR SEQ ID NO:23:

50	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 280 amino acids
	(B) TYPE: amino acid
	(D) TOPOLOGY: linear
55	(ii) MOLECULE TYPE: protein
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
60	Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
	-26 -25 -20 -15
	Leu Val Leu Leu Pro Val Thr Ser Ser Asp Arg Met Lys Gln Ile Glu
	-10 -5 1 5

	Asp	Lys	Ile	Glu	Glu	Ile	Leu	Ser	Lys	Ile	Tyr	His	Ile	Glu	Asn	Glu	
				10					15					20			
5	Ile	Ala	Arg	Ile	Lys	Lys	Leu	Ile	Gly	Glu	Arg	Thr	Ser	Ser	Asp	Tyr	
			25					30					35				
	Lys	Asp	Asp	Asp	Asp	Lys	Asp	Lys	Val	Glu	Glu	Glu	Val	Asn	Leu	His	
		40					45					50					
10	Glu	Asp	Phe	Val	Phe	Ile	Lys	Lys	Leu	Lys	Arg	Cys	Asn	Lys	Gly	Glu	
		55				60					65					70	
	Gly	Ser	Leu	Ser	Leu	Leu	Asn	Cys	Glu	Glu	Met	Arg	Arg	Gln	Phe	Glu	
15					75					80					85		
	Asp	Leu	Val	Lys	Asp	Ile	Thr	Leu	Asn	Lys	Glu	Glu	Lys	Lys	Glu	Asn	
				90					95					100			
20	Ser	Phe	Glu	Met	Gln	Arg	Gly	Asp	Glu	Asp	Pro	Gln	Ile	Ala	Ala	His	
			105					110					115				
	Val	Val	Ser	Glu	Ala	Asn	Ser	Asn	Ala	Ala	Ser	Val	Leu	Gln	Trp	Ala	
			120				125					130					
25	Lys	Lys	Gly	Tyr	Tyr	Thr	Met	Lys	Ser	Asn	Leu	Val	Met	Leu	Glu	Asn	
		135				140					145					150	
	Gly	Lys	Gln	Leu	Thr	Val	Lys	Arg	Glu	Gly	Leu	Tyr	Tyr	Val	Tyr	Thr	
30					155					160					165		
	Gln	Val	Thr	Phe	Cys	Ser	Asn	Arg	Glu	Pro	Ser	Ser	Gln	Arg	Pro	Phe	
				170					175					180			
35	Ile	Val	Gly	Leu	Trp	Leu	Lys	Pro	Ser	Ser	Gly	Ser	Glu	Arg	Ile	Leu	
			185					190					195				
	Leu	Lys	Ala	Ala	Asn	Thr	His	Ser	Ser	Ser	Gln	Leu	Cys	Glu	Gln	Gln	
		200					205					210					
40	Ser	Val	His	Leu	Gly	Gly	Val	Phe	Glu	Leu	Gln	Ala	Gly	Ala	Ser	Val	
		215				220					225					230	
	Phe	Val	Asn	Val	Thr	Glu	Ala	Ser	Gln	Val	Ile	His	Arg	Val	Gly	Phe	
45					235					240					245		
	Ser	Ser	Phe	Gly	Leu	Leu	Lys	Leu									
				250													